RAW SEQUENCE LISTING ERROR REPORT
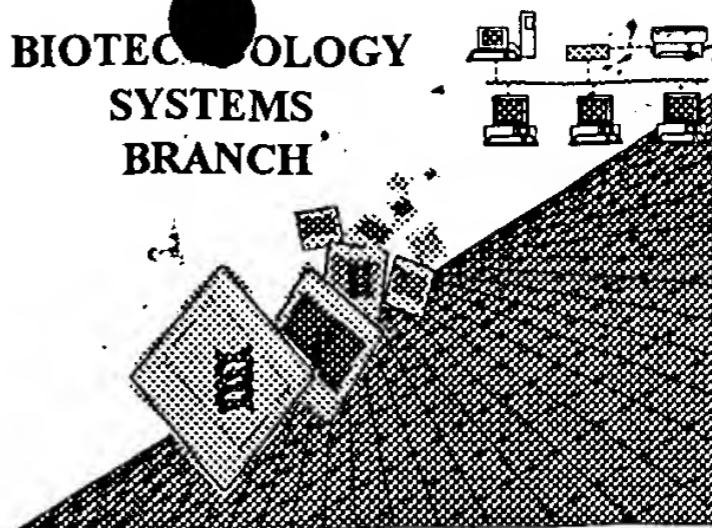
BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/829, 066A_

Source: _OIPE_

Date Processed by STIC: _8/2/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/829,066A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length.

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) 10 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING   DATE: 08/02/2001
PATENT APPLICATION: **US/09/829,066A** TIME: 10:02:44

Input Set : **A:\seqlist_09424800001.txt**
Output Set: **N:\CRF3\08022001\I829066A.raw**

Does Not Comply
Corrected Diskette Needed
gg 1-6

```
 4 <110> APPLICANT: Nisson, Paul
 5        Jesse, Joel
 6        Li, Wu-bo
 8 <120> TITLE OF INVENTION: Method for Isolating and Recovering Target DNA or RNA
 9        Molecules Having a Desired Nucleotide Sequence
11 <130> FILE REFERENCE: 0942.4800002/RWE/ALS
14 <140> CURRENT APPLICATION NUMBER: US 09/829,066A
15 <141> CURRENT FILING DATE: 2001-04-10
17 <150> PRIOR APPLICATION NUMBER: US 09/103,577
18 <151> PRIOR FILING DATE: 1998-06-24
20 <150> PRIOR APPLICATION NUMBER: US 60/050,729
21 <151> PRIOR FILING DATE: 1997-06-25
23 <160> NUMBER OF SEQ ID NOS: 12
25 <170> SOFTWARE: PatentIn version 3.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 23
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: degenerate oligonucleotide
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: 3
40 <223> OTHER INFORMATION: where n is g, t, a, or c
42 <220> FEATURE:
43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: 12
45 <223> OTHER INFORMATION: where n is g, t, a, or c
47 <220> FEATURE:
48 <221> NAME/KEY: misc_feature
49 <222> LOCATION: 21
50 <223> OTHER INFORMATION: where n is g, t, a, or c
52 <400> SEQUENCE: 1
53 gtn tgy gay ggn tty cay gtn gg                              23
57 <210> SEQ ID NO: 2
58 <211> LENGTH: 23
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
63 <223> OTHER INFORMATION: degenerate oligonucleotide
65 <220> FEATURE:
66 <221> NAME/KEY: misc_feature
67 <222> LOCATION: 3
68 <223> OTHER INFORMATION: where n is (dK)
70 <220> FEATURE:
71 <221> NAME/KEY: misc_feature
72 <222> LOCATION: 6
```

PSI: "n can only represent a single nucleotide, nothing else"

```
 73 <223> OTHER INFORMATION: where n is (dP)
 75 <220> FEATURE:
 76 <221> NAME/KEY: misc_feature
 77 <222> LOCATION: 9
 78 <223> OTHER INFORMATION: where n is (dP)
 80 <220> FEATURE:
 81 <221> NAME/KEY: misc_feature
 82 <222> LOCATION: 12
 83 <223> OTHER INFORMATION: where n is (dK)
 85 <220> FEATURE:
 86 <221> NAME/KEY: misc_feature
 87 <222> LOCATION: 15
 88 <223> OTHER INFORMATION: where n is (dP)
 90 <220> FEATURE:
 91 <221> NAME/KEY: misc_feature
 92 <222> LOCATION: 18
 93 <223> OTHER INFORMATION: where n is (dP)
 95 <220> FEATURE:
 96 <221> NAME/KEY: misc_feature
 97 <222> LOCATION: 21
 98 <223> OTHER INFORMATION: where n is (dK)
100 <400> SEQUENCE: 2
101 gtn tgn gan ggn ttn can gtn gg                          23
105 <210> SEQ ID NO: 3
106 <211> LENGTH: 23
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: degenerate oligonucleotide
113 <220> FEATURE:
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: 3
116 <223> OTHER INFORMATION: where n is (dK)
118 <220> FEATURE:
119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: 6
121 <223> OTHER INFORMATION: where n is (dP)
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: 9
126 <223> OTHER INFORMATION: where n is (dP)
128 <220> FEATURE:
129 <221> NAME/KEY: misc_feature
130 <222> LOCATION: 12
131 <223> OTHER INFORMATION: where n is (dK)
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature
135 <222> LOCATION: 15
136 <223> OTHER INFORMATION: where n is (dP)
```

W-->

```
        138 <220> FEATURE:
        139 <221> NAME/KEY: misc_feature
        140 <222> LOCATION: 18
        141 <223> OTHER INFORMATION: where n is dP
        143 <220> FEATURE:
        144 <221> NAME/KEY: misc_feature
        145 <222> LOCATION: 21
        146 <223> OTHER INFORMATION: where n is dP
        148 <400> SEQUENCE: 3
W-->    149 gtn tgn gan ggn ttn can gtn gg                          23
        153 <210> SEQ ID NO: 4
        154 <211> LENGTH: 23
        155 <212> TYPE: DNA
        156 <213> ORGANISM: Artificial Sequence
        158 <220> FEATURE:
        159 <223> OTHER INFORMATION: degenerate oligonucleotide
        161 <220> FEATURE:
        162 <221> NAME/KEY: misc_feature
        163 <222> LOCATION: 3
        164 <223> OTHER INFORMATION: where n is dK
        166 <220> FEATURE:
        167 <221> NAME/KEY: misc_feature
        168 <222> LOCATION: 6
        169 <223> OTHER INFORMATION: where n is dP
        171 <220> FEATURE:
        172 <221> NAME/KEY: misc_feature
        173 <222> LOCATION: 9
        174 <223> OTHER INFORMATION: where n is dP
        176 <220> FEATURE:
        177 <221> NAME/KEY: misc_feature
        178 <222> LOCATION: 12
        179 <223> OTHER INFORMATION: where n is dP
        181 <220> FEATURE:
        182 <221> NAME/KEY: misc_feature
        183 <222> LOCATION: 15
        184 <223> OTHER INFORMATION: where n is dP
        186 <220> FEATURE:
        187 <221> NAME/KEY: misc_feature
        188 <222> LOCATION: 18
        189 <223> OTHER INFORMATION: where n is dP
        191 <220> FEATURE:
        192 <221> NAME/KEY: misc_feature
        193 <222> LOCATION: 21
        194 <223> OTHER INFORMATION: where n is dK
        196 <400> SEQUENCE: 4
W-->    197 gtn tgn gan ggn ttn can gtn gg                          23
        201 <210> SEQ ID NO: 5
        202 <211> LENGTH: 23
        203 <212> TYPE: DNA
```

```
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: degenerate oligonucleotide
209 <220> FEATURE:
210 <221> NAME/KEY: misc_feature
211 <222> LOCATION: 3
212 <223> OTHER INFORMATION: where n is dP
214 <220> FEATURE:
215 <221> NAME/KEY: misc_feature
216 <222> LOCATION: 6
217 <223> OTHER INFORMATION: where n is dP
219 <220> FEATURE:
220 <221> NAME/KEY: misc_feature
221 <222> LOCATION: 9
222 <223> OTHER INFORMATION: where n is dP
224 <220> FEATURE:
225 <221> NAME/KEY: misc_feature
226 <222> LOCATION: 12
227 <223> OTHER INFORMATION: where n is dK
229 <220> FEATURE:
230 <221> NAME/KEY: misc_feature
231 <222> LOCATION: 15
232 <223> OTHER INFORMATION: where n is dP
234 <220> FEATURE:
235 <221> NAME/KEY: misc_feature
236 <222> LOCATION: 18
237 <223> OTHER INFORMATION: where n is dP
239 <220> FEATURE:
240 <221> NAME/KEY: misc_feature
241 <222> LOCATION: 21
242 <223> OTHER INFORMATION: where n is dK
244 <400> SEQUENCE: 5
245 gtn tgn gan ggn ttn can gtn gg                              23
249 <210> SEQ ID NO: 6
250 <211> LENGTH: 23
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: degenerate oligonucleotide
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: 3
260 <223> OTHER INFORMATION: where n is dP
262 <220> FEATURE:
263 <221> NAME/KEY: misc_feature
264 <222> LOCATION: 6
265 <223> OTHER INFORMATION: where n is dP
267 <220> FEATURE:
268 <221> NAME/KEY: misc_feature
```

```
269 <222> LOCATION: 9
270 <223> OTHER INFORMATION: where n is dP
272 <220> FEATURE:
273 <221> NAME/KEY: misc_feature
274 <222> LOCATION: 12
275 <223> OTHER INFORMATION: where n is dK
277 <220> FEATURE:
278 <221> NAME/KEY: misc_feature
279 <222> LOCATION: 15
280 <223> OTHER INFORMATION: where n is dP
282 <220> FEATURE:
283 <221> NAME/KEY: misc_feature
284 <222> LOCATION: 18
285 <223> OTHER INFORMATION: where n is dP
287 <220> FEATURE:
288 <221> NAME/KEY: misc_feature
289 <222> LOCATION: 21
290 <223> OTHER INFORMATION: where n is dP
292 <400> SEQUENCE: 6
```
-> **293 gtn tgn gan ggn ttn can gtn gg**   23
```
297 <210> SEQ ID NO: 7
298 <211> LENGTH: 23
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: degenerate oligonucleotide
305 <220> FEATURE:
306 <221> NAME/KEY: misc_feature
307 <222> LOCATION: 3
308 <223> OTHER INFORMATION: where n is dK
310 <220> FEATURE:
311 <221> NAME/KEY: misc_feature
312 <222> LOCATION: 6
313 <223> OTHER INFORMATION: where n is dP
315 <220> FEATURE:
316 <221> NAME/KEY: misc_feature
317 <222> LOCATION: 9
318 <223> OTHER INFORMATION: where n is dP
320 <220> FEATURE:
321 <221> NAME/KEY: misc_feature
322 <222> LOCATION: 12
323 <223> OTHER INFORMATION: where n is dP
325 <220> FEATURE:
326 <221> NAME/KEY: misc_feature
327 <222> LOCATION: 15
328 <223> OTHER INFORMATION: where n is dP
330 <220> FEATURE:
331 <221> NAME/KEY: misc_feature
332 <222> LOCATION: 18
```

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

```
<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence
```
see item 11 on Eua Summary Sheet

```
<400> 10
gac cgt tca gct gga tat tac ggc c                                    25
```

Input Set : **A:\seqlist_09424800001.txt**
Output Set: **N:\CRF3\08022001\I829066A.raw**

```
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:446 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:446 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
```